

Neutrokin- α

1 AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGAC 60
 61 ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC 120
 121 CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC 180
 1 M D D S T E R E Q S R L 12
 181 TTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAACTGAAGGAGTGTGTTTCCATCCTCC 240
 13 T S C L K K R E E M K L K E C V S I L P 32
 CD-I
 241 CACGGAAGGAAAGCCCTCTGTCCGATCCTCCAAAGACGGAAGCTGCTGGCTGCAACCT 300
 33 R K E S P S V R S S K D G K L L A A T L 52
 CD-I
 301 TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCC 360
 53 L L A L L S C C L T V V S F Y Q V A A L 72
 361 TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC 420
 73 Q G D L A S L R A E L Q G H H A E K L P 92
 CD-II
 421 CAGCAGGAGCAGGAGCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC 480
 93 A G A G A P K A G L E E A P A V T A G L 112
 CD-III
 481 TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA 540
 113 K I F E P P A P G E G N S S Q N S R N K 132
 #
 541 AGCGTGCCGTTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG 600
 133 R A V Q G P E E T V T Q D C L Q L I A D 152
 CD-IV

FIG.1A

Neutrokin- α

601	ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT	660
153	S E T P T I Q K G S Y T F <u>V P W L L S F</u>	172
	CD-V	
661	TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTT	720
173	<u>K R G S A L E E K</u> E N K <u>I L V K E T G Y</u>	192
	CD-V	CD-VI
721	ACTTTTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAA	780
193	<u>F F I Y G Q V L Y T D K T Y A M G H L I</u>	212
	CD-VI	CD-VII
781	TTCAGAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT	840
213	<u>Q R K K V H V F G D E L S L V T L F R C</u>	232
	CD-VII	CD-VIII
	#	
841	GTATTCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAA	900
233	<u>I Q N M P E T L P N N S C Y S A G I A K</u>	252
	CD-VIII	CD-IX
901	AACTGGAAGAAGGAGATGAACTCCAACCTTGCAATACCAAGAGAAAATGCACAAATATCAC	960
253	<u>L E E G D E L Q L A I P R E N A Q I S L</u>	272
	CD-X	
961	TGGATGGAGATGTCACATTTTTTGGTGCATTGAACTGCTGTGACCTACTTACACCATGT	1020
273	D G D V <u>T F F G A L K L L</u>	285
	CD-XI	
1021	CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA	1080
1081	CCAAAAAAAAAAAAAAAAAAAAA	1100

FIG.1B

	10	20	30	
1	M S T E S M I R D V E L	- - - - -	- - - A E E A	TNFalpha
1	M - - - - -	- - - - -	- - - T P P E R L	TNFbeta
1	M G A - - - - -	- - - - -	- - - - -	LTbeta
1	M Q Q P F N Y P Y P Q I Y W -	V D S S A S S P W A P P G T V	- - - - -	FasLigand
1	M D D S T E R E Q S R L	T S C L K K R E E M K L	K E C V S I	Neutrokine alpha
1	M D D S T E R E Q S R L	T S C L K K R E E M K L	K E C V S I	Neutrokine alphaSV
	40	50	60	
17	L P K K T G G P Q - - G S R R -	- - - - -	- - - - -	TNFalpha
8	F - - - - -	- - - - -	- - - - -	TNFbeta
4	- - - L G L E G R G G -	- - - - -	- - - - -	LTbeta
30	L P C P T S V P R R P G Q R R P P P P P P P P P P P P P P P	- - - - -	- - - - -	FasLigand
31	L P R K E S P S V R S S K D - -	G K L L A A T L L L A L L	- - - - -	Neutrokine alpha
31	L P R K E S P S V R S S K D - -	G K L L A A T L L L A L L	- - - - -	Neutrokine alphaSV
	70	80	90	
30	- - - - -	- - - - -	C L F L S L F S	TNFalpha
9	- - - - -	L P R V R G T T L H L L L G L L V L L P	- - - - -	TNFbeta
12	- - - - -	- R L Q G R G S L L L A V A G A T S L V T	- - - - -	LTbeta
60	P P P L P P P L P P P L K K R G N H S T G L C L L V M F F M	- - - - -	- - - - -	FasLigand
58	S C C L T V V S F Y Q V A A L Q G D L A S L R A E L Q G H H	- - - - -	- - - - -	Neutrokine alpha
58	S C C L T V V S F Y Q V A A L Q G D L A S L R A E L Q G H H	- - - - -	- - - - -	Neutrokine alphaSV

	100										110										120										
38	F	L	-	-	I	V	A	G	A	T	T	L	F	C	L	L	H	F	G	V	I	G	P	Q	R	E	E	F	F	P	R
31	G	A	Q	G	L	P	G	V	G	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
32	L	L	A	V	P	I	T	V	L	A	V	L	A	L	V	P	Q	D	Q	G	G	L	V	T	E	T	A	D	P	-	
90	V	L	V	A	L	V	G	L	G	L	G	M	F	Q	L	F	H	L	Q	K	E	L	A	E	L	R	E	S	T	S	
88	A	E	K	L	P	A	G	A	G	A	P	K	A	G	L	E	E	A	P	A	V	T	A	G	L	K	I	F	E	P	
88	A	E	K	L	P	A	G	A	G	A	P	K	A	G	L	E	E	A	P	A	V	T	A	G	L	K	I	F	E	P	

	130	140	150
66	DLSLIS - PLA - QA VRSSSRTPSD - - KPVA		
41	- - T P S - AAQ - TA RQH PKMHLAHS TLKPAA		
62	GAQAQQ - GLGFQKLPEEEPETDLSPLGLPAA		
120	QMHTAS - SLE - KQIGH P S P P P E K K E L R K V A		
118	PAPGEGNSSSQNSRRNKRAVQGPPEETVTQDCL		
118	PAPGEGNSSSQNSRRNKRAVQGPPEET - - - -		

	160	170	180
91	H V A N P Q A E G - Q	- - - - -	L Q W L N R R A N A L L
66	H L I G D P S K Q N - S	- - - - -	L L W R A N T D R A F L
91	H L I G A P L K - G Q G	- - - - -	L G W E T T K E Q A F L
148	H L T G K S N S R S M P -	- - - - -	L E W E D T Y G I V L L
148	Q L I A D S E T P T I Q	K G S Y T F F V P W L	- - - L S F K
142	- - - - -	G S Y T F F V P W L	- - - L S F K

FIG. 2B

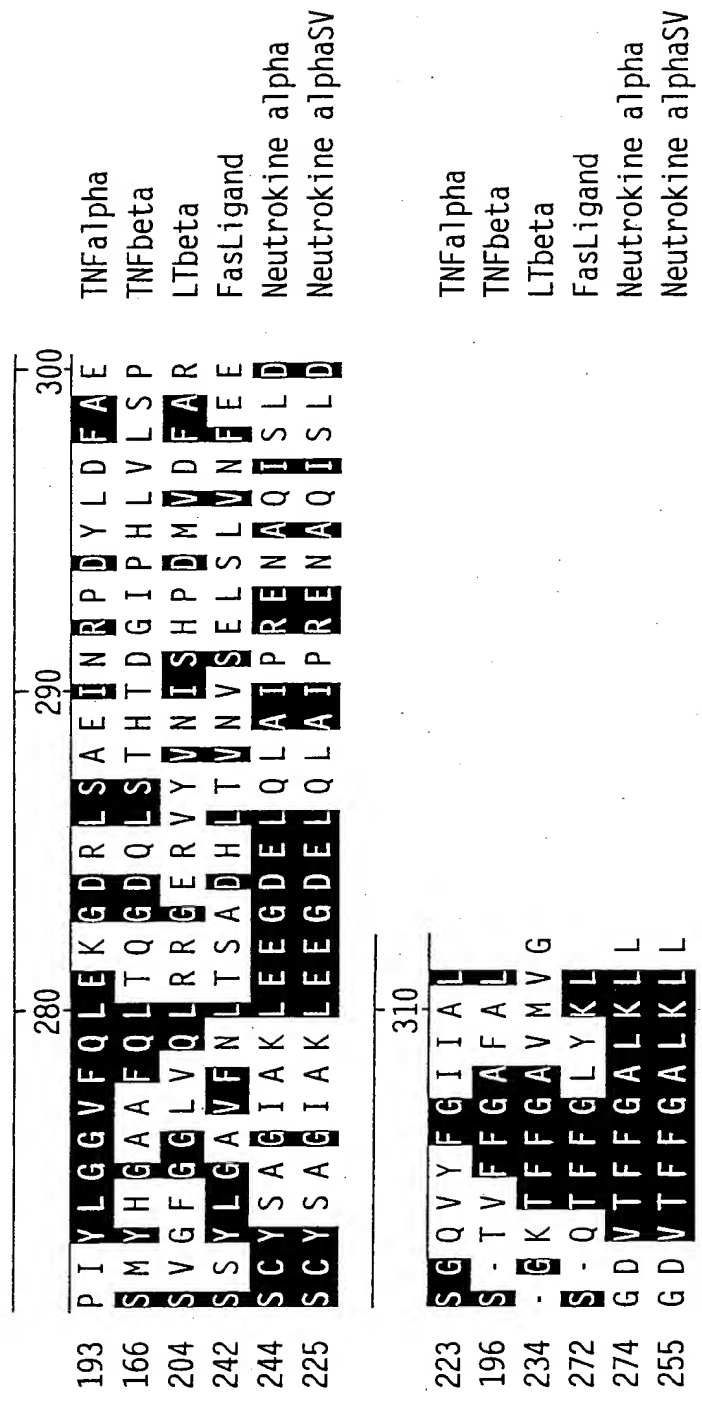
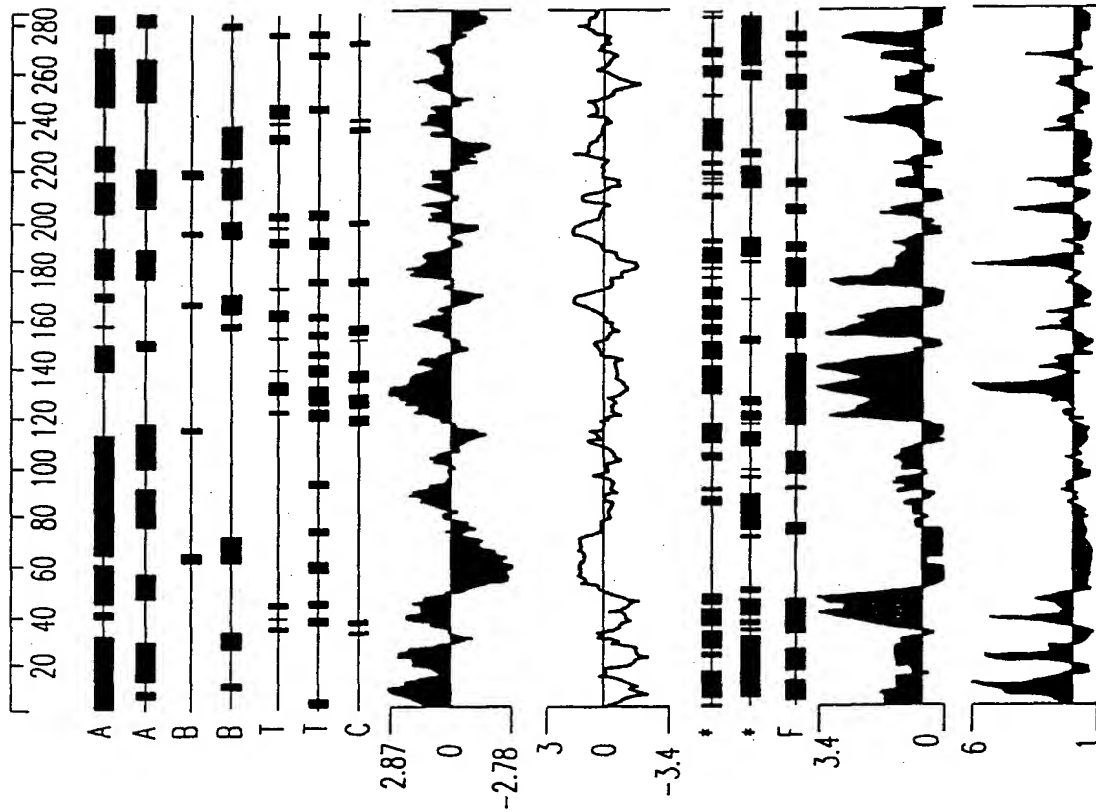


FIG.2D

NEUTROKINE- α



■ ALPHA, REGIONS-GARNIER-ROBSON
 ■ ALPHA, REGIONS-CHOU-FASMAN
 ■ BETA, REGIONS-GARNIER-ROBSON
 ■ BETA, REGIONS-CHOU-FASMAN
 ■ TURN, REGIONS-GARNIER-ROBSON
 ■ TURN, REGIONS-CHOU-FASMAN
 ■ COIL, REGIONS-GARNIER-ROBSON

■ HYDROPHILICITY PLOT-KYTE-DOOLITTLE

□ HYDROPHOBICITY PLOT-HOPP-WOODS

■ ALPHA, AMPHIPATHIC REGIONS-EISENBERG
 ■ BETA, AMPHIPATHIC REGIONS-EISENBERG
 ■ FLEXIBLE REGIONS-KARPLUS-SCHULZ

■ ANTIGENIC INDEX-JAMESON-WOLF

■ SURFACE PROBABILITY PLOT-EMINI

FIG.3

	1		50
HSOAD55RA GGNTAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA		
HNEDU15X	...AAATTCA GGATAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA		
HSLAH84R	.AATTCGGCA NAGNAACTG GTTACTTTTT TATATATGGT CAGGTTTTAT		
HLTBM08R	AATTCGGCAC GAGCAAGGCC GGCCTGGAGG AAGCTCCAGC TGTCACCGCG		
	51		100
HSOAD55R	GTGCACGCAG GACATCANCA A..ACACANN NNNCAGGAAA TAATCCATTC		
HNEDU15X	GTGCACGCAG GACATCAACA A..ACACAGA TAACAGGAAA TGATCCATTC		
HSLAH84R	ATACTGATAA GACCTACGCC ATGGGACATC TAGTTCAGAG GAAGAAGGTC		
HLTBM08R	GGACTGAAAA TCTTTGAACC ACCAGCTCCA GGAGAAGGCA ACTCCAGTCA		
	101		150
HSOAD55R	CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA		
HNEDU15X	CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA		
HSLAH84R	CATGTCTTTG GGGATGAATT GAGTCTGGTG ACTTTGTTTC GATGTATTCA		
HLTBM08R	GAACAGCAGA AATAAGCGTG CCGTTCAGGG TCCAGAAGAA ACAGTCACTC		
	151		200
HSOAD55R	TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA		
HNEDU15X	TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA		
HSLAH84R	AAATATGCCT GAAACACTAC CCAATAATTC CTGCTATTCA GCTGGCATTG		
HLTBM08R	AAGACTGCTT GCAACTGNNT GCAGACAGTG AAACACCAAC TATACAAAAA		
	201		250
HSOAD55R	AGAAAAGAGA AGAAATGAAA CTGNAAGGAG TGTGTTTCCA TCCTCCCACG		
HNEDU15X	AGAAAAGAGA AGAAATGAAA CT.GAAGGAG TGTGTTTCCA TCCTCCCACG		
HSLAH84R	CAAAACTGGN AGGAAGGA.. ...GATGAAC TCCAAC TTGC AATACCAGGG		
HLTBM08R	GGCTCCCTTC TGNTGCCACA TTTGGGCCAA GGAATGGAGA GATTTCTTCG		
	251		300
HSOAD55R	GAAGGAAAGC CCCTCTNTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG		
HNEDU15X	GAAGGAAAGC CCCTCTGTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG		
HSLAH84R	GAAAATGCAC AATTATCACT GGGATGGAGA TGTTACATT TTTTGGGTGC		
HLTBM08R	TCTGGAAACA TTTTGCCAAA CTCTTCAGAT ACTCTTNTCT CTCTGGGAAT		
	301		350
HSOAD55R	CAACCTTGNT GNTGGCATTG TGTTCTTGCT GNCTCAAGGT GGTGTTNTT.		
HNEDU15X	CAACCTTGCT GCTGGCACTG CTGTCTTGCT GCCTCACGGT GGTGTCTTTC		
HSLAH84R	CATTGAACT GCTGTGACCT NCTTACANCA NGTGCTGTTN GCTATTTTNC		
HLTBM08R	CAAAGGAAAA TCTCTACTTA GATTNACACA TTTGTTCCCA TGGGTNTCTT		
	351		400
HSOAD55R		
HNEDU15X	TACCAGGTGG CCGCCCTGCA AGGGGACCTG GCCAGCCTCC GGGCAGAGCT		
HSLAH84R	CTNCCTNTTC TNTGGTAACC TCTTAGGAAG GAAGGATTCT TAACTGGGAA		
HLTBM08R	AAGTTTTAAA AGGGGAGTGC CCTTAGGAGG AAAAGGGGAT AAATATTGGC		

FIG.4A

	401		450
HSOAD55R
HNEDU15X	GCAGGGCCAC	CACGCGGAGA	AGCTGCCAGC
HSLAH84R	ATAACCCAAA	AAAANNTTAA	ANGGGTANGN
HLTBM08R	CAAGGNACTG	GTTANTTTNT	AAATATGGTC
		AGGTTTNTAT	ANCTGGTAGG
	451		500
HSOAD55R
HNEDU15X	CCGGCCTGGA	GGAAGCTCCA	GCTGTCACCG
HSLAH84R	CNNGNNGNNT	TTTNGGNNTA	TNTTNTNNTN
HLTBM08R	CCTCGCCATG	GGCATTNATT	CANGGNGAGG
		NCNNTCTTTT	GGGNTGA...
	501		550
HSOAD55R
HNEDU15X	CCACCAGCTC	CAGGAGAAGG	CAACTCCAGT
HSLAH84R	CNANGGGGGN	TTTTT.....
HLTBM08R
	551		600
HSOAD55R
HNEDU15X	TGCCGTTTCA	GGTCCAGAAG	AAACAGTCAC
HSLAH84R
HLTBM08R
	601		650
HSOAD55R
HNEDU15X	TTGCAGACAG	TGAAACACCA	ACTATACAAA
HSLAH84R
HLTBM08R
	651		700
HSOAD55R
HNEDU15X	CCATGGCTTC	TCAGCTTTAA	AAGGGGAAGT
HSLAH84R
HLTBM08R
	701		750
HSOAD55R
HNEDU15X	TAAAATATTG	GTCAAAGAAA	CTGGTTACTT
HSLAH84R
HLTBM08R
	751		800
HSOAD55R
HNEDU15X	TATATACTGA	TAAGACCTAC	GCCATGGGAC
HSLAH84R
HLTBM08R

FIG.4B

	801		850
HSOAD55R
HNEDU15X	GTCCATGTCT	TTGGGGATGA	ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R
HLTBM08R
	851		900
HSOAD55R
HNEDU15X	TCAAAATATG	CCTGAAACAC	TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R
HLTBM08R
	901		950
HSOAD55R
HNEDU15X	TTGCAAAACT	GGAAGAAGGA	GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R
HLTBM08R
	951		1000
HSOAD55R
HNEDU15X	AATGCACAAA	TATCACTGGA	TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R
HLTBM08R
	1001		1050
HSOAD55R
HNEDU15X	ACTGCTGTGA	CCTACTTACA	CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R
HLTBM08R
	1051		1100
HSOAD55R
HNEDU15X	CTGTACCTCT	AAGAAGAAAG	AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R
HLTBM08R
	1101		
HSOAD55R		
HNEDU15X	AAAAAA		
HSLAH84R		
HLTBM08R		

FIG.4C

Neutrokin- α SV

1	ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA	60
1	M D D S T E R E Q S R L T S C L K K R E	20
61	GAAATGAACTGAAGGAGTGTGTTTCCATCCTCCACGGAAGGAAAGCCCCTCTGTCCGA	120
21	E M K L K E C V S I <u>L P R K E S P S V R</u>	40
	CD-I	
121	TCCTCCAAAGACGGAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC	180
41	<u>S S K D G K L L A A T L L L A L L S C C</u>	60
	CD-I	
181	CTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG	240
61	<u>L T V V S F Y Q V A A L Q G D L A S L R</u>	80
	CD-II	
241	GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCAAGGCC	300
81	<u>A E L Q G H H A E K L P A G A G A P K A</u>	100
	CD-II	CD-III
301	GGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA	360
101	<u>G L E E A P A V T A G L K I F E P P A P</u>	120
	CD-III	
	#	
361	GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTCCAGGGTCCAGAAGAA	420
121	G E G N S S Q N S R N K R A V Q G P E E	140
421	ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA	480
141	T G S Y T F <u>V P W L L S F K R G S A L E</u>	160
	CD-IV	
481	GAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTACTTTTTTATATATGGTCAGGTT	540
161	<u>E K E N K I L V K E T G Y F F I Y G Q V</u>	180
	CD-IV	CD-V
541	TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC	600
181	<u>L Y T D K T Y A M G H L I Q R K K V H V</u>	200
	CD-VI	CD-VII

FIG.5A

Neutrokin- α SV

601 TTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAAATATGCCTGAAACA 660
201 F G D E L S L V T L F R C I Q N M P E T 220
CD-VIII CD-VIII

661 CTACCCAATAATTCCTGCTATTTCAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACTC 720
221 L P N N S C Y S A G I A K L E E G D E L 240
CD-IX CD-X

721 CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT 780
241 Q L A I P R E N A Q I S L D G D V T F F 260
CD-X CD-XI

781 GGTGCATTGAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCCTCCCTTTC 840
261 G A L K L L 266
CD-XI

841 TCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAAAAA 900

901 AAA 903

FIG.5B

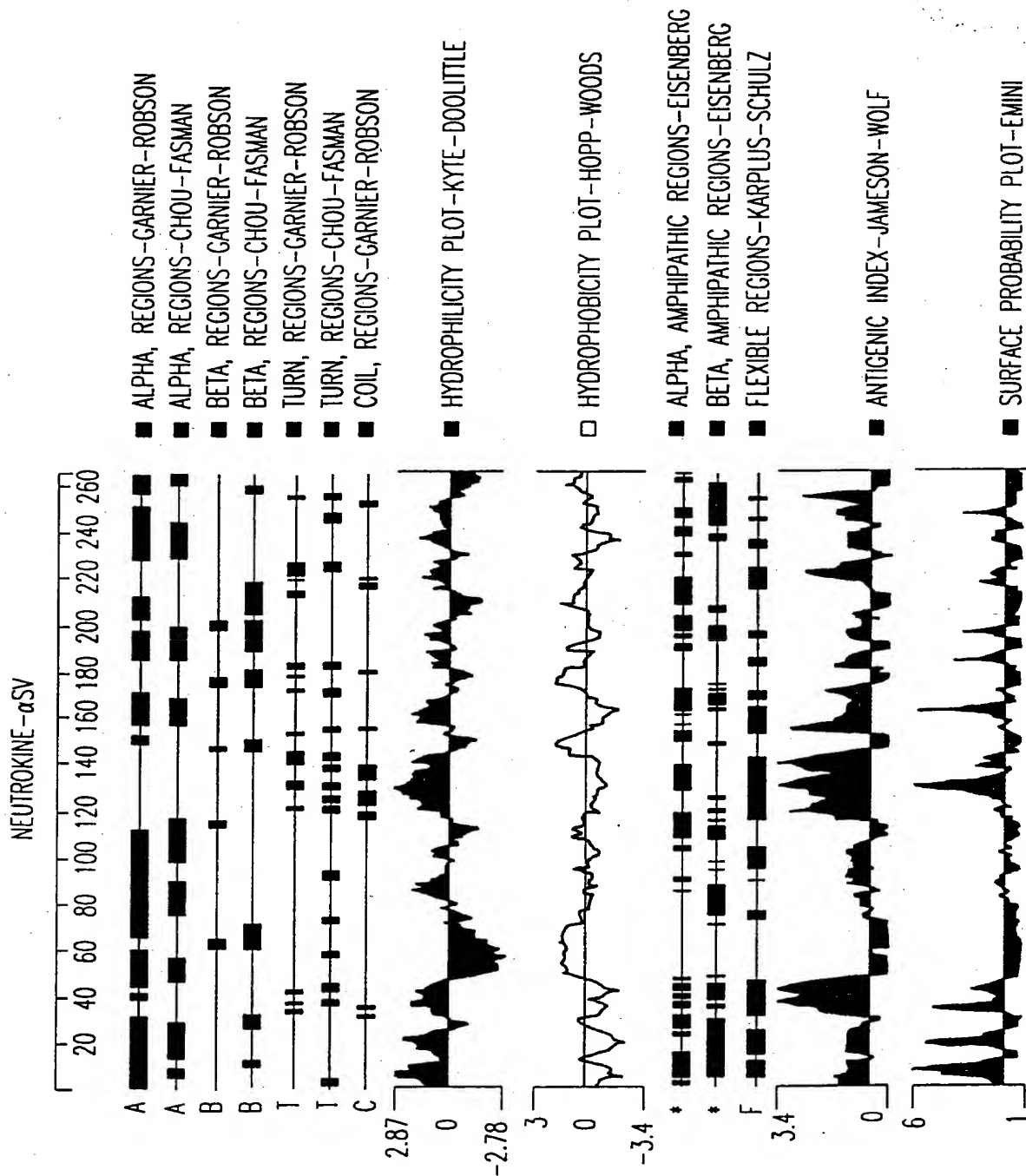


FIG.6

Neutrokin-

Alpha MDDSTEREQSRLTSCCLKKREEMKLKECVSILPRKESPSVRS 41

Transmembrane Region

SKDGKLLAATLLALLSCCLTVVSFYQVAALQGDLASLRAE 82

LQGHHAELPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEG 123

↓

NSSQNSRNKRAVQGP EETVT QDC QLIAD SE PTIQKGS Y T 164
 Apr1l H SVL H LV P I N A T SK - DDSDV T 134
 TNF K PVA H VV A N P Q A E G Q - - - - - 102
 LT α K PAA H LI G DP S K Q N S - - - - - 76

FVPWL L S - - - - F K R G S A L E E K E N K I L V K E T G Y F F F I Y G Q V L 200
 EV M W Q P A - - - - L R R G R G L Q A Q G Y G V R I Q D D A G V Y L L Y S Q V L 170
 - L Q W L N R R A N A L L A N G V E L R D - - N Q L V V P S E G L Y L I Y S Q V L 139
 - L L W R A N T D R A F L Q D G F S L S N - - N S L L V P T S G I Y F V Y S Q V V 114

Y T D K T Y - - - - A M G H L I Q R K K V H V F G D E L S L V T L F R C I Q N M P 237
 F Q D V T F - - - - T M G Q V V S R E - - - - G Q G R Q E T L F R C I R S M P 201
 F K G Q G C P - - - - S T H V L L T H I S R I A V S V Q T K V N L L S A I K S P 176
 F S G K A Y S P K A T S S P L Y L A H E V Q L F S S Q V P F H V P L L S S Q K M V 155

FIG.7A-1

FIG. 7A-2

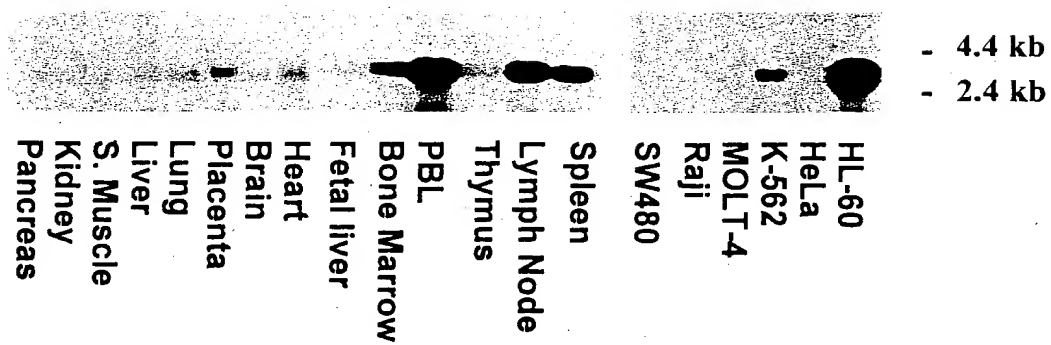


FIG. 7B

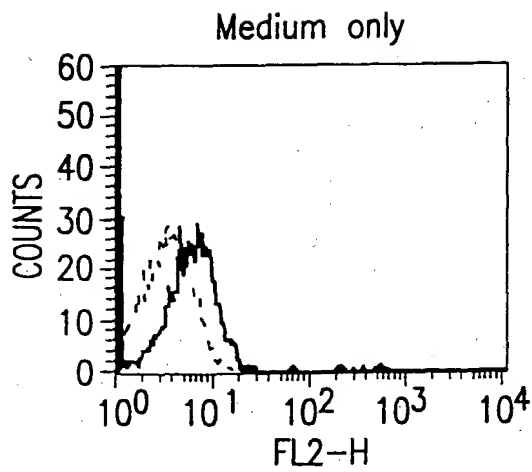


FIG.8A

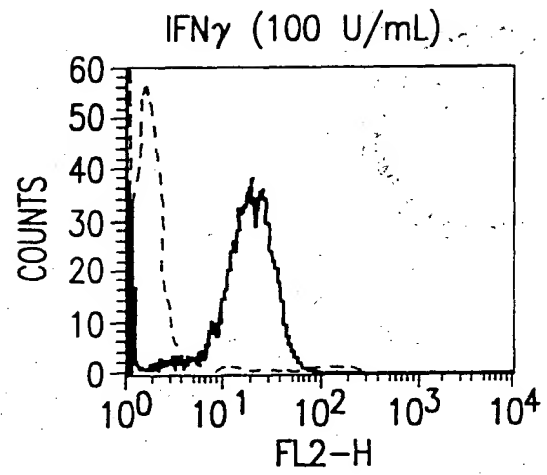


FIG.8B

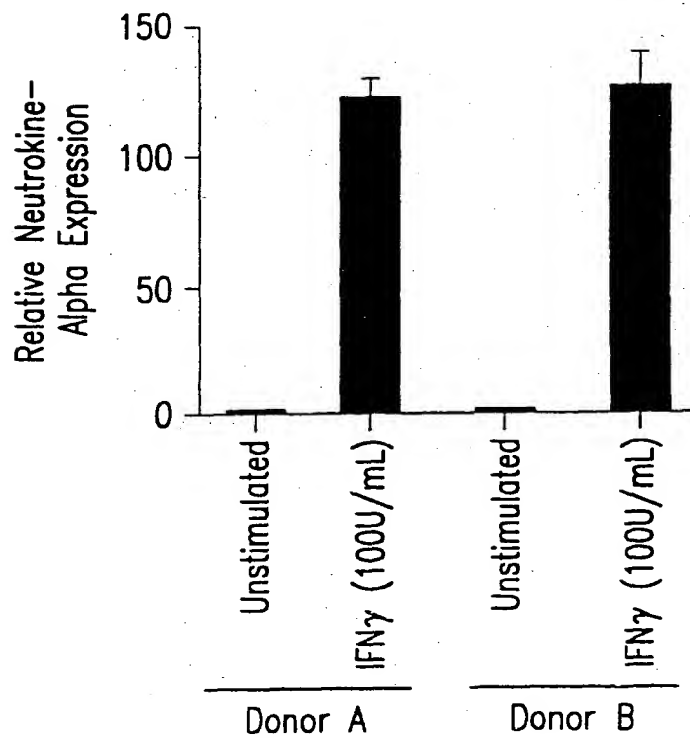


FIG.8C

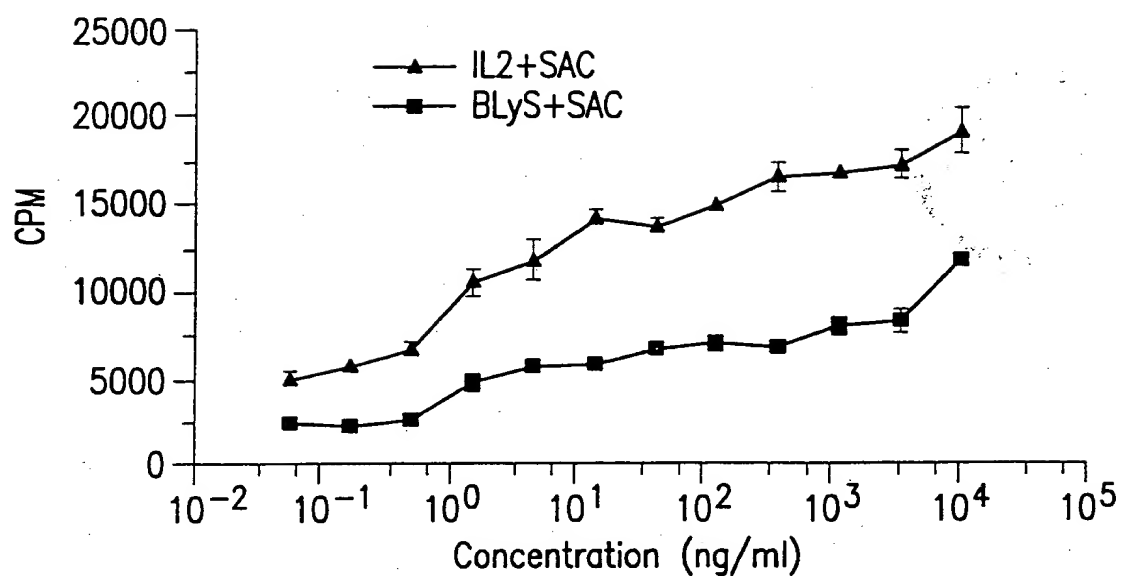


FIG. 9A

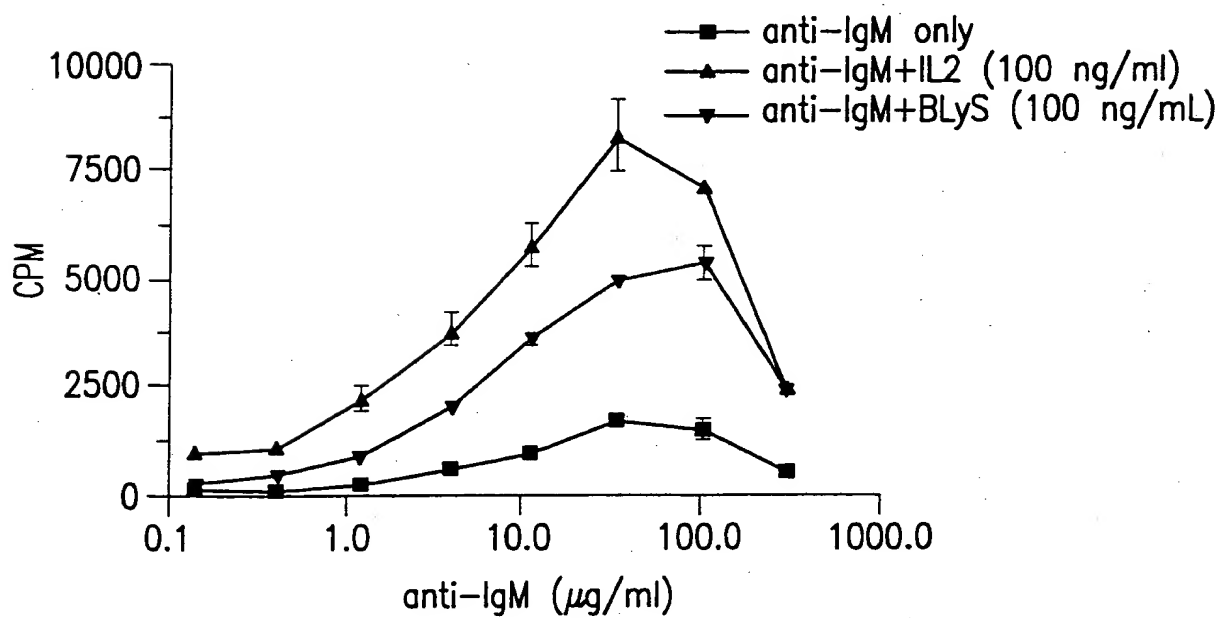


FIG. 9B

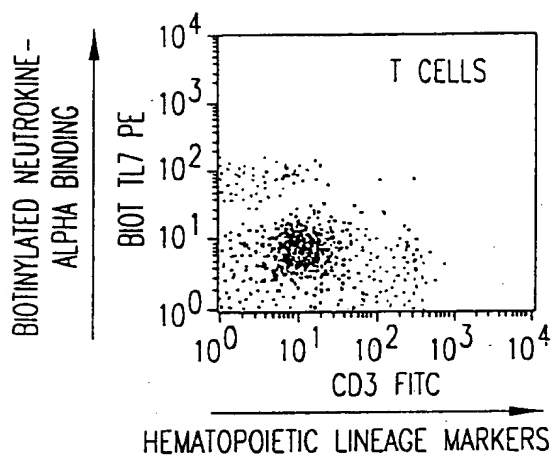


FIG.10A

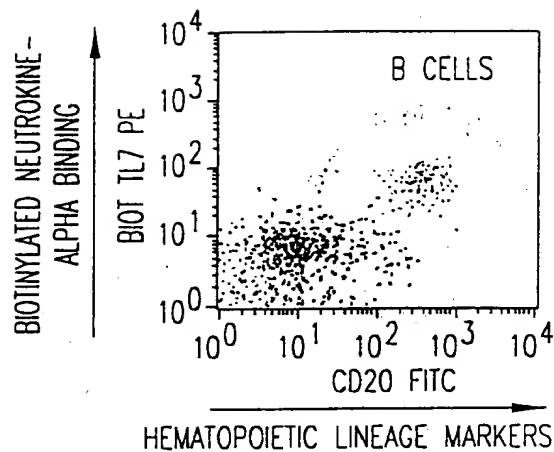


FIG.10B

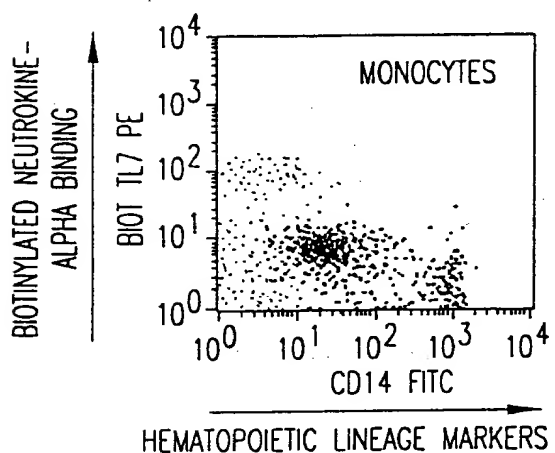


FIG.10C

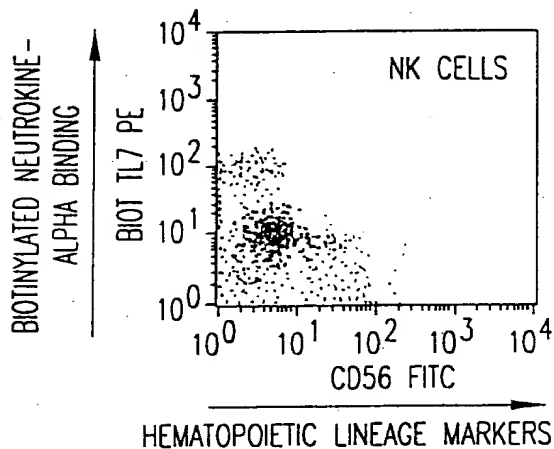


FIG.10D

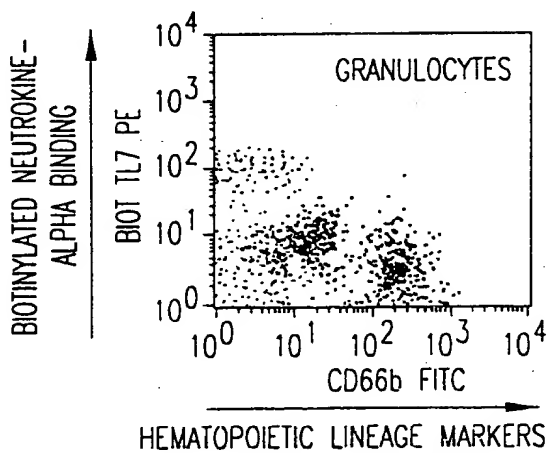


FIG.10E

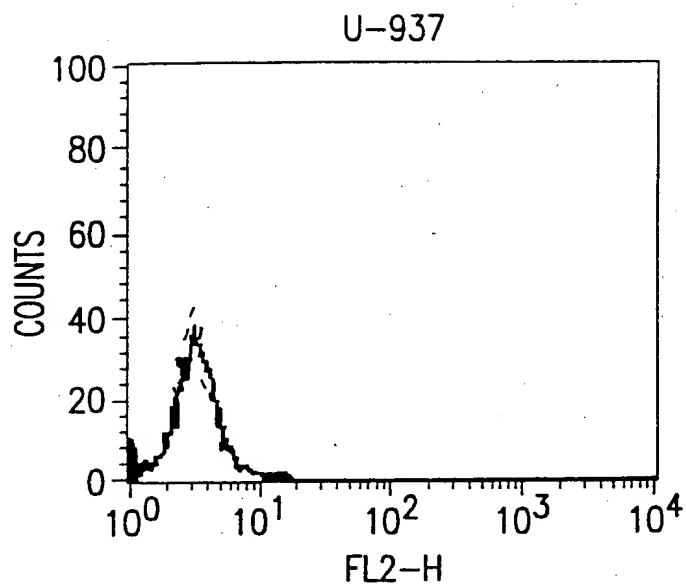


FIG.10F

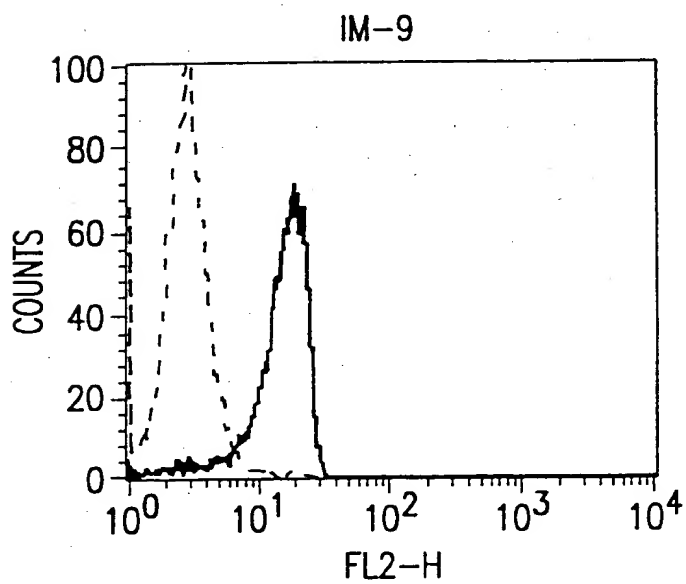
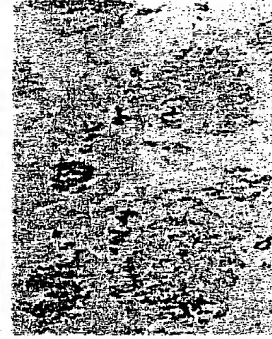
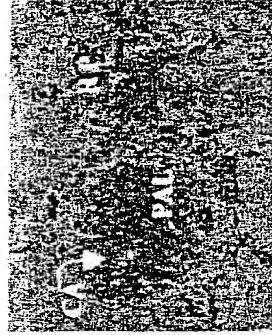


FIG.10G

530 351

Neutrokine - alpha
treated spleen
(2mg/Kg) bid 4d

Normal spleen



H & E (100X)

CD45R(B220)
(40X)



FIG.11A

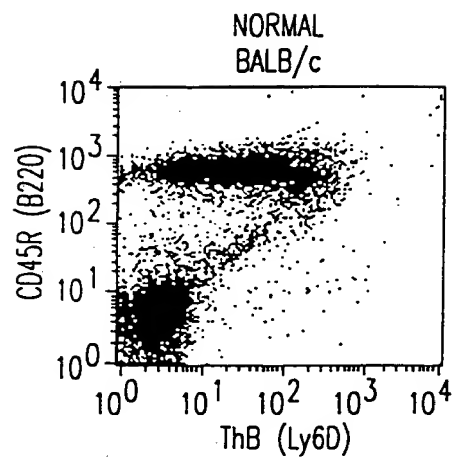


FIG. 11B

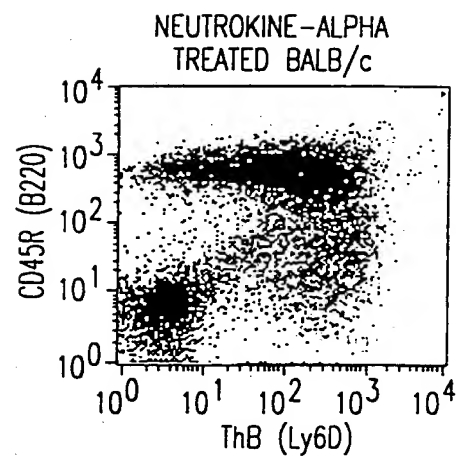


FIG. 11C

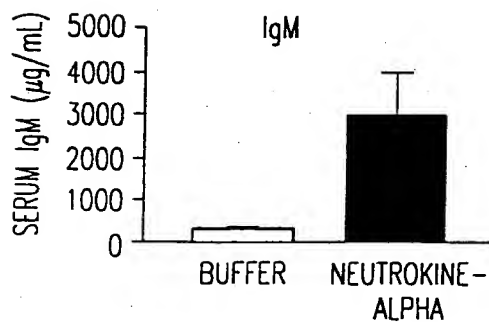


FIG. 11D

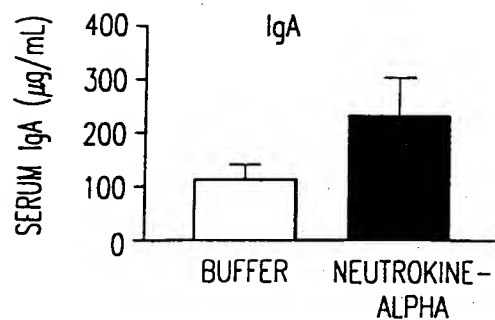


FIG. 11E

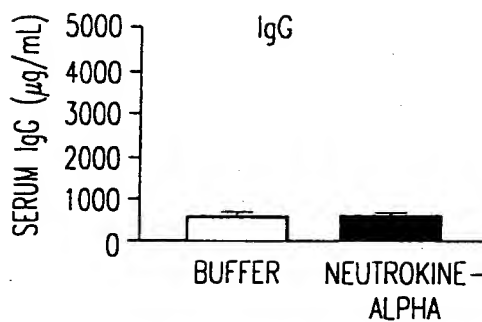


FIG. 11F

Figure 7

a.

leutokine-

alpha MDDSTEREQSRLTSCCLKKREEMKLKECVSILPRKESPSVRS 41

Transmembrane Region

SKD G K L L A A T L L L A L L S C C L T V V S F Y Q V A A L G D L A S L R A E 82

L Q G H H A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P P A P G E G 123

N S S Q N S R N K R A V Q G P E E T V T Q D C L Q L A D S E T P T I Q K G S Y T 164

April H S V L H L V P I N A T S K - D D S D V T 134

TNF K P V A H V V A N P Q A E G Q - - - - - 102

LT α K P A A H L T G D P S K Q N S - - - - - 77

F V P W E L S - - - - F K R G S A L E E K E N K I L V K E T G Y F F I Y G O V E 200

E V M W Q P A - - - - L R R G R G L Q A Q G Y G V R I Q D A G V Y L L Y S O V L 170

- L Q W L N R R A N A L L A N G V E L R D - - N Q L V V P S E G L Y L I Y S O V L 139

- L L W R A N T D R A F L Q D G F S L S N - - N S L L V P T S G I Y F V Y S O V V 114

Y T D K T Y - - - - A M G H L I Q R K K V H V E G D E L S L V T L F R C I O N M P 237

Q D V T F - - - - M G O V V S R E - - - - G G R Q E T L F R C I R S M P 201

K G Q G C P - - - - S T H V L L T H T I S R I A V S Y Q T K V N L L S A I K S P 176

S G K A V S P K A F S S P Y L A E V Q L E S S Q V P F H V P L L S S O R K M V 155

E - - T L P - - - - - N N S C Y S A G I A K L E E G D E L Q L A I P R E N A 268

S H P D R A - - - - - Y N S C Y S A G V F H L H Q C D I L S V I L P R A R A 234

C Q R E T P E G A E A K P W Y E P I N L G G V F O L E K G D R L S A E I N R P D Y 217

Y P - - - - - G L Q E P W L H S M X H G A A F O L T Q G D Q L S T H T D G I P H 190

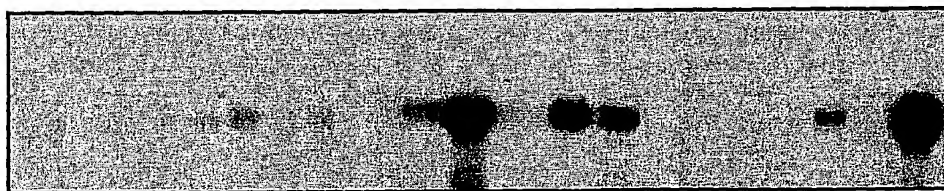
Q I S E D G D V T F F G A L K L L 285

K L N I S P H G T F L G F V K L 250

E D F A E S G Q V Y E G I I A T 233

E V L S - E S T V F E G A F A L 205

b.



4.4 kb

2.4 kb

HL-60
HeLa
K-562
MOLT-4
Raji
SW480
Spleen
Lymph Node
Thymus
PBL
Bone Marrow
Fetal liver
Heart
Brain
Placenta
Lung
Liver
S. Muscle
Kidney
Pancreas

DELETE PORTION OF LINE IN BRACKET

change "77" to "76"

"G" at position 197 should be black text on white background